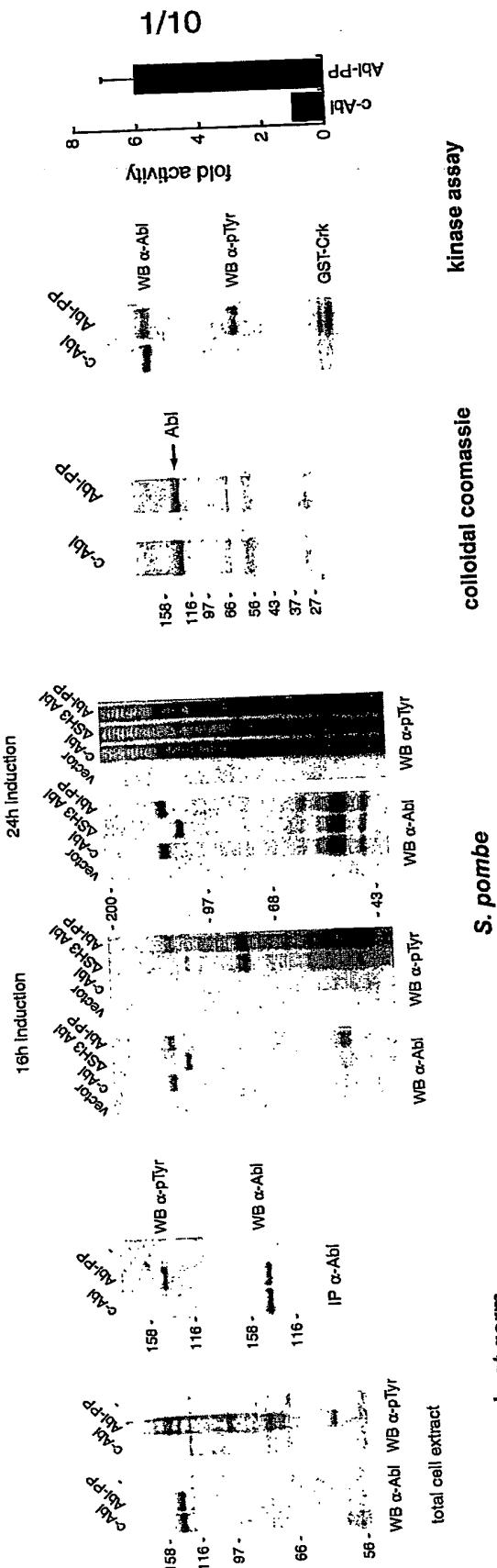


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正

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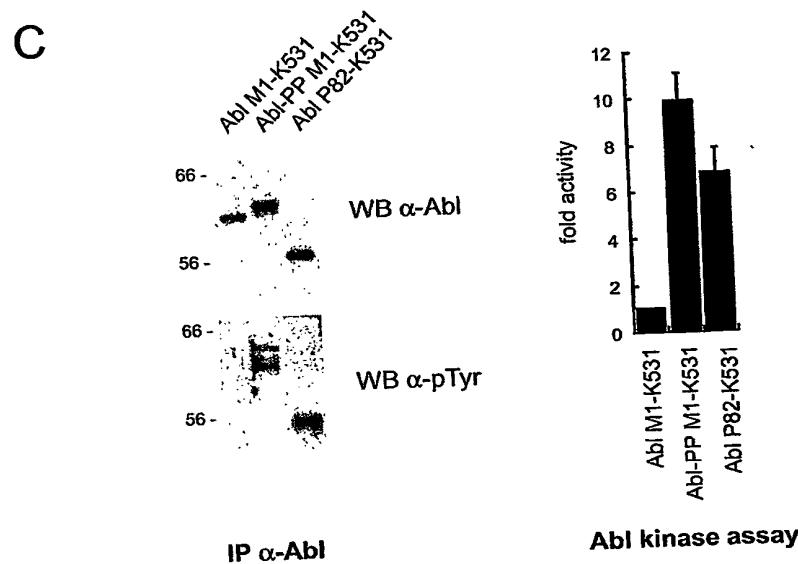
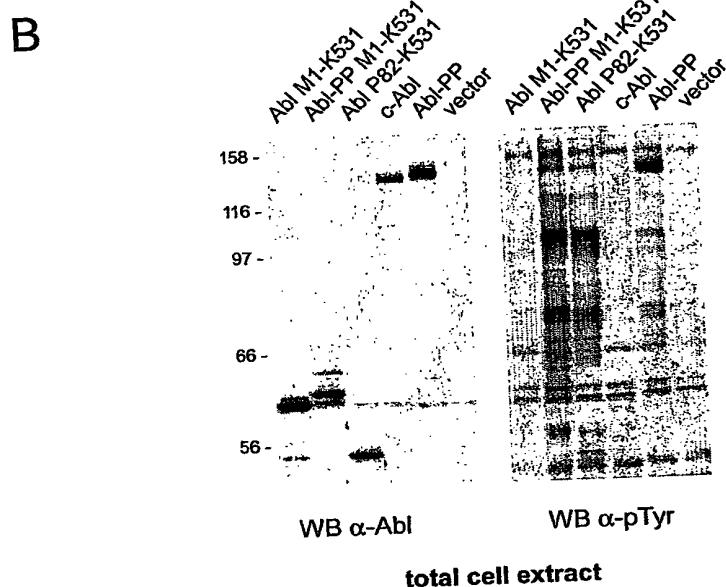
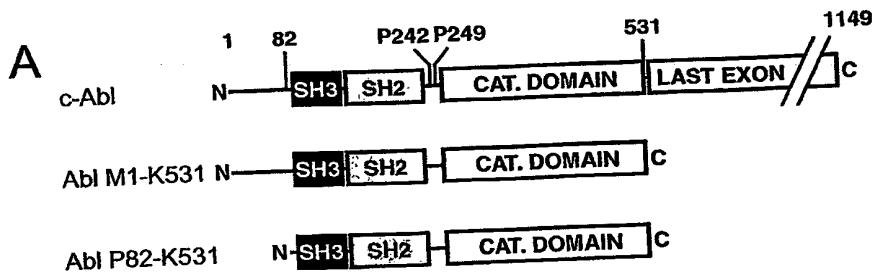
5



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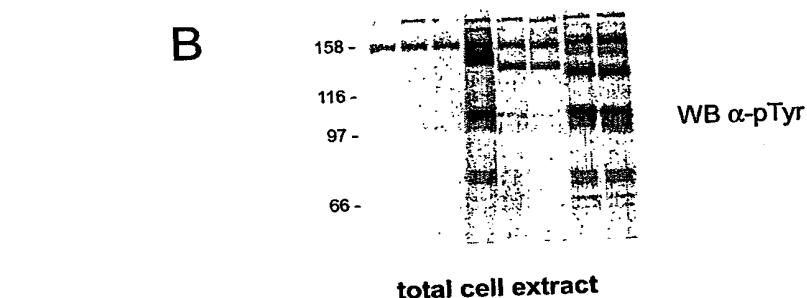
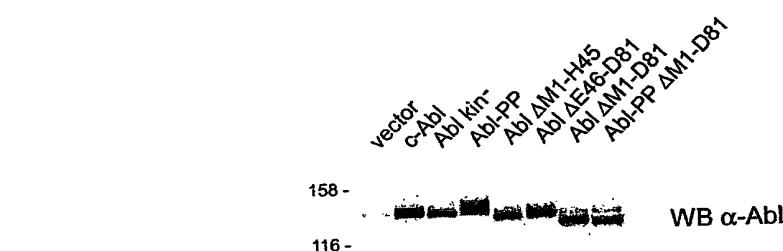
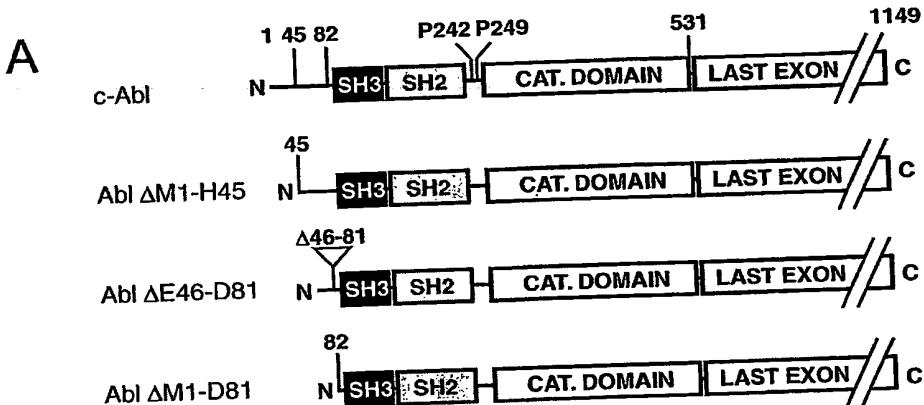
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FIG. 2

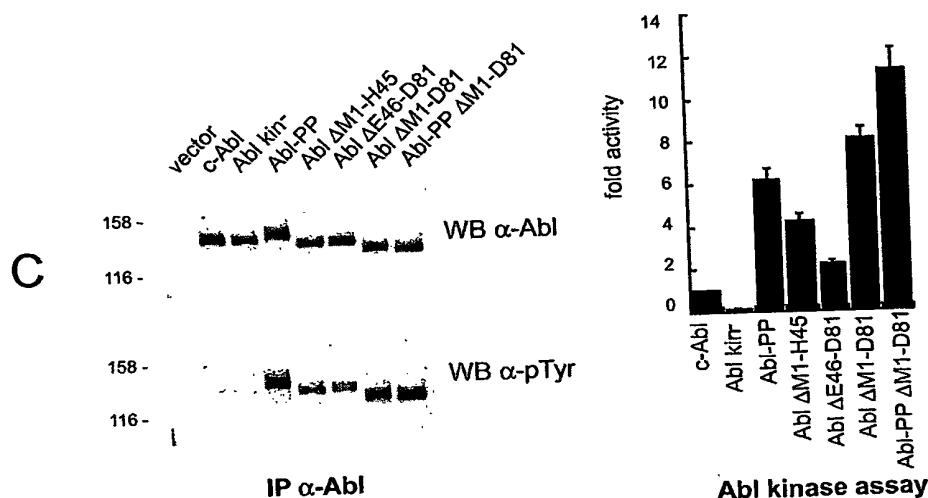


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FIG. 3



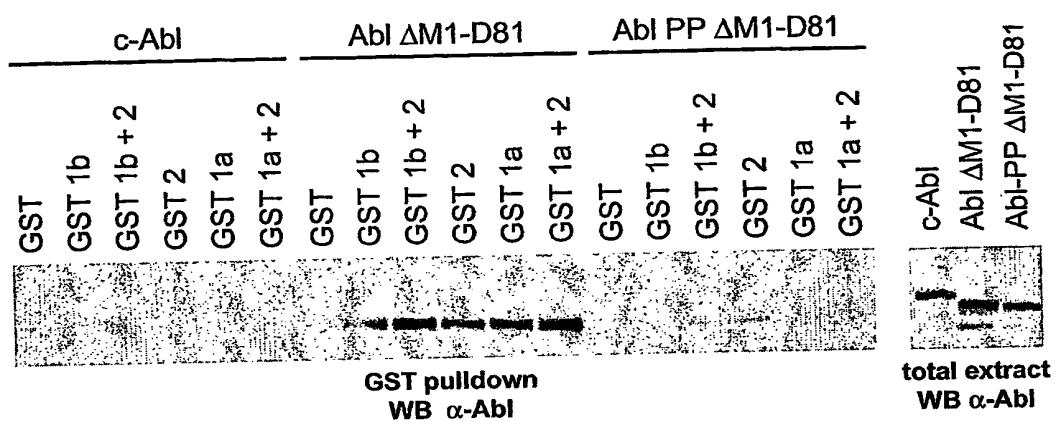
total cell extract



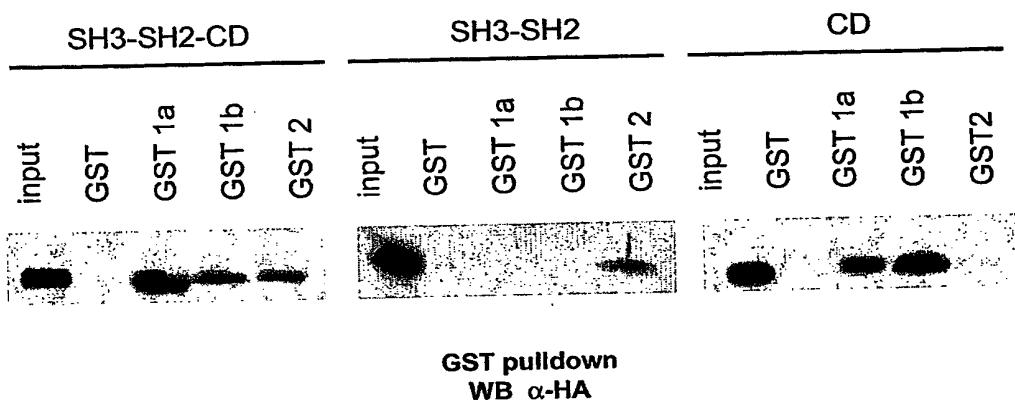
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FIG. 4

A



B



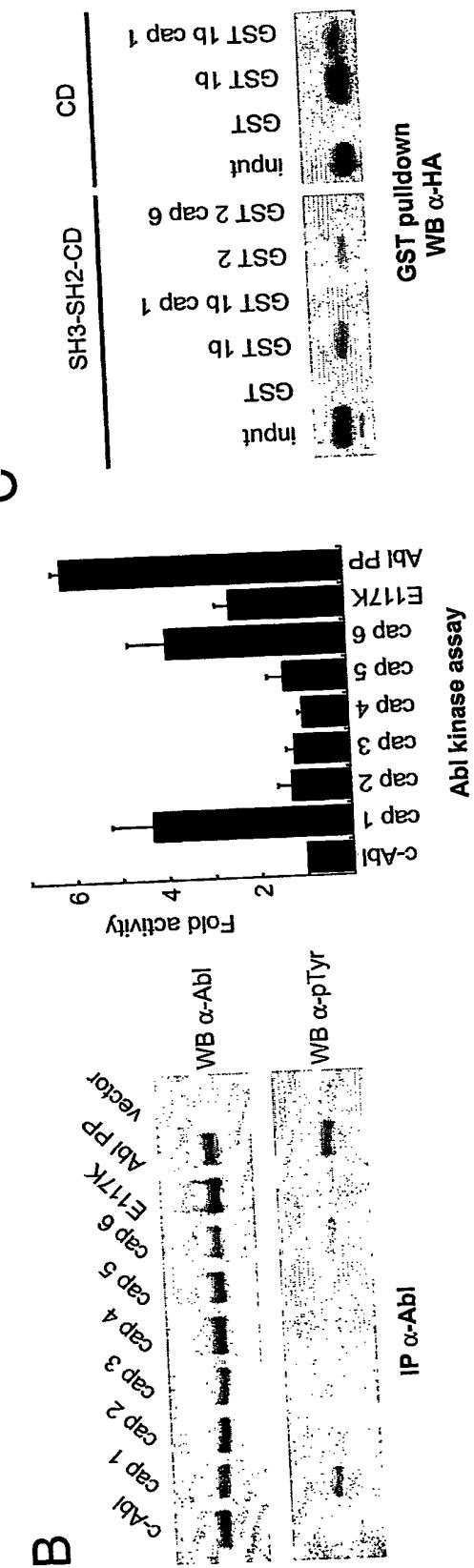
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boundary 1st/2nd exon

Ab1 1b 1MGQQPGKVLGDDQRRPSLPAALHFIKGACKRDSRHGGPHCNVFVEHEALQRPVASDFEPQGLSEARWNSKENLLAGPSEN80

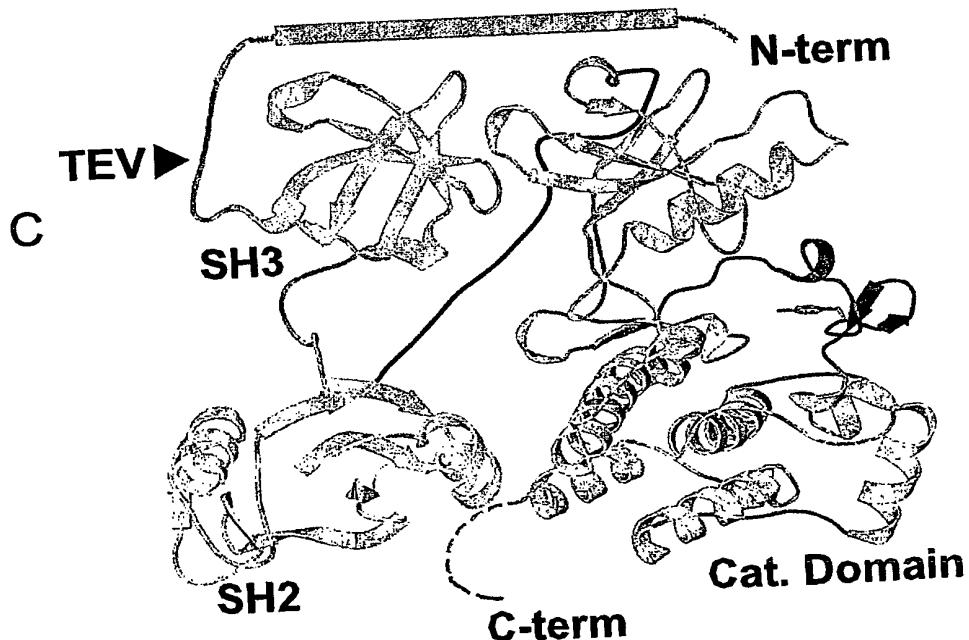
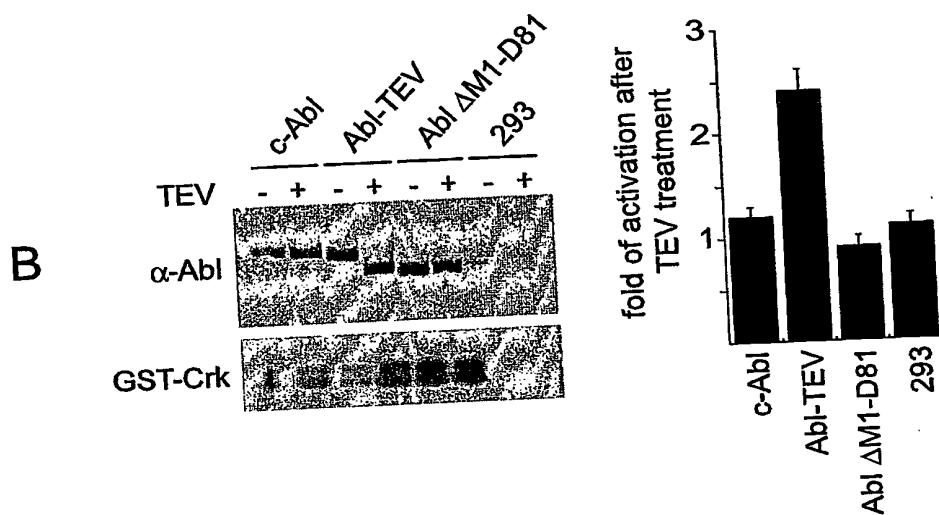
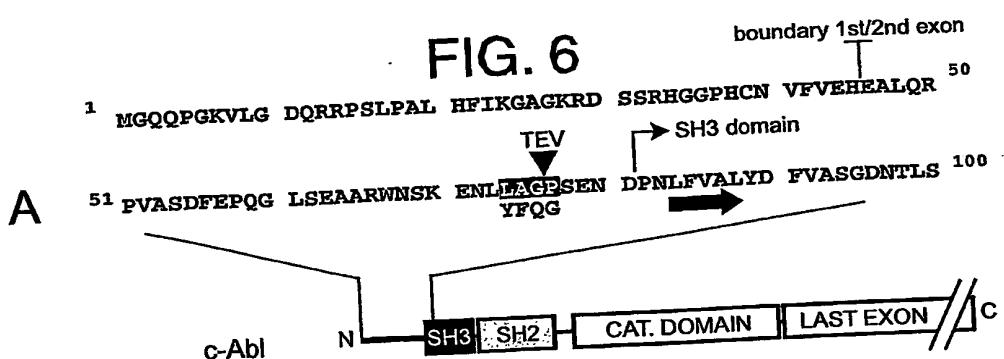
Ab1 1a 1MLEICKLKVGCKSK-----KGLS-----SS-----



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FIG. 6



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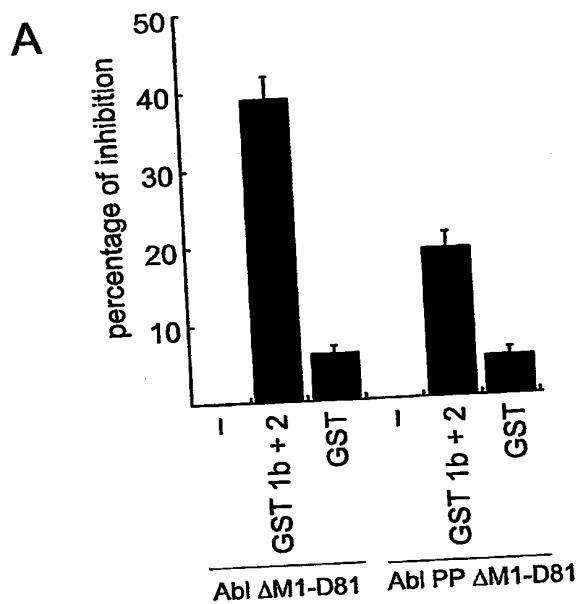
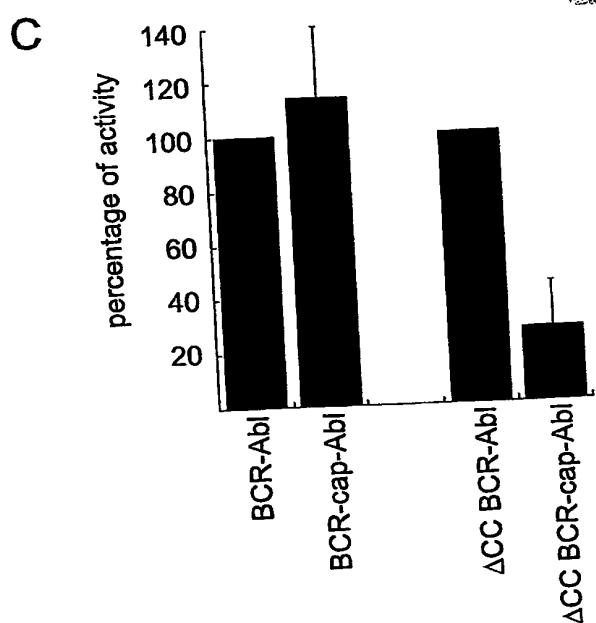
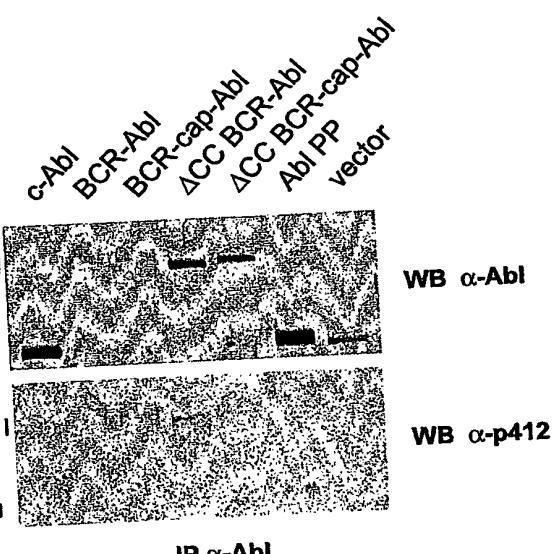


FIG. 7



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FIG 8

hAb11a	MLEICLKL-----VGCKSK-----KGLSSSSS-----	C-YLEE-----
mAb1I	MLEICLKL-----VGCKSK-----KGLSSSSS-----	C-YLEEH-----
hAb11b	MGQQPGKV-----LGDQRRPSLPALHFIKGAGKRDSSRHGGP-----	HCNVFVEH-----
mAb1IV	MGQQPGKV-----LGDQRRPSLPALHFIKGAGKRDSSRHGGP-----	HCNVFVEH-----
hArg1a	--MVLGTV-----LLPPN-----TYGRDQDTS-----	LCCLCTEA-----
hArg1b	MGQQVGRVGEAPGLQQPQPRGIRGSSAARPSGRRDPAGRTTETGFNIFTQHDHFASCVED	
hAb11a	-----ALQRPVASDFEPQGLSEAARWNS <u>KENLLAGPSEN</u> -----	61
mAb1I	-----EALQRPVASDFEPQGLSEAARWNS <u>KENLLAGPSEN</u> -----	63
hAb11b	-----EALQRPVASDFEPQGLSEAARWNS <u>KENLLAGPSEN</u> -----	92
mAb1IV	-----EALQRPVASDFEPQGLSEAARWNS <u>KENLLAGPSEN</u> -----	80
hArg1a	---SESALPDLTEALHRYGCDVEPQALNEAIRWSS <u>KENLLGATES</u> -----	71
hArg1b	GFE GDKTGGSSPEALHRYGCDVEPQALNEAIRWSS <u>KENLLGATES</u> -----	107

Legend:**Bold:** cap 1 domainUnderlined: cap 6 domain

Bold italic: conserved domain upstream of cap 6 domain that forms an alpha helix with cap 6 domain

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FIG 9

hAb11a	-----
mAb1I	-----
hAb11b	-----
mAb1IV	-----
hArg	ATGGGGCAGCAGGTGGCCGCGTCGGGAAGCTCCGGGCTCCAGCAGCCTCAGCCCCGC 60

hAb11a	-----
mAb1I	-----
hAb11b	-----ATGGGGCAGCAGCCTGGAAAAGTTCTTGGGACCAAAG 38
mAb1IV	-----ATGGGGCAGCAGCCTGGAAAAGTTCTTGGGACCAAAG 38
hArg	GGGATCCGGGGCAGCAGTGCAGCCAGGCCCTCCGGCCGCAGGCGGGACCCGGCGGGCGC 120

hAb11a	-----ATGTTGGAGATCTGCCTGAAGCTGGTGGCTGCAAATCCAAGAAGG 46
mAb1I	-----ATGTTGGAGATCTGTTGAAGTTGGTGGCTGCAAATCCAAGAAGG 46
hAb11b	AAGGCCTAGTTGCCCGCCCTGCATTTATCAAAGGGCAGGGAAGAGGGACTCATCGAG 98
mAb1IV	AAGGCCTAGTTGCCCGCCCTGCATTTATCAAAGGGCAGGGAAGAGGGACTCATCGAG 98
hArg	ACCACAGAGACCGGTTCAATATCTCACCCAGCATGATCACTTGCCAG-CTGTGTGGA 179

hAb11a	GGCTGTCCTCGTCCTCCAGCTGTTATCTGGAAGAA-----GCCCTGCAGAGGCCAGT 98
mAb1I	GGCTCTTCGTCCTCCAGCTGCTACCTGGAGGAACAC--GAAGCCCTGCAGAGGCCAGT 104
hAb11b	GCATGGGGC-CCACACTGCAATGTCTTGTGGAACAC--GAAGCCCTGCAGAGGCCAGT 155
mAb1IV	GCATGGGGC-CCACACTGCAATGTCTTGTGGAACAC--GAAGCCCTGCAGAGGCCAGT 155
hArg	GGATGGATTTGAGGGAGACAAGACTGGAGGCAGTAGTCCAGAAGCTTGATCGTCCCTA 239

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hAb11a GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 158
mAb1I GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 164
hAb11b GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 215
mAb1IV GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 215
hArg TGGTTGTGATGTTGAACCCCAGGCACTAAATGAGGCTATCAGGTGGAGCTCCAAGGAGAA 299

hAb11a CCTTCTTGCTGGGCCAGTGAAAAT----- 183
mAb1I CCTTCTTGCTGGGCCAGTGAAAAT----- 189
hAb11b CCTTCTTGCTGGGCCAGTGAAAATGACCCAACCTTTGTGGCACTCTATGATTTGT 275
mAb1IV CCTTCTTGCTGGGCCAGTGAAAAT----- 240
hArg CTTGCTCG---GAGCCACTGAGAGTGACCCTAAT----- 330

hAb11a -
mAb1I -
hAb11b G 276
mAb1IV -
hArg -